

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 18:00:15 ; Search time 15 Seconds
(without alignments)
96.134 Million cell updates/sec

Title: US-09-300-612-1
Perfect score: 84
Sequence: 1 LKAMDPTPLWKTE 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB	ID	Description
1	63	75.0	237	2	A42013		alpha-1-B-glycoprotein
2	46	54.8	1213	2	A54063		TATA-binding prote
3	44	52.4	695	2	E75099		hypothetical prote
4	44	52.4	777	2	T38769		hypothetical prote
5	44	52.4	1327	2	T09402		immunoglobulin-lik
6	43	51.2	341	2	AB0644		probable glycosyl
7	43	51.2	687	2	D86314		hypothetical prote
8	43	51.2	932	1	A31898		hydroxymethylgluta
9	42	50.0	115	2	D71194		hypothetical prote
10	42	50.0	398	2	A81717		hypothetical prote
11	42	50.0	453	2	T04646		conserved hypothet
12	42	50.0	564	1	VHXPMV		aspartate transami
13	42	50.0	662	2	A29900		major structural n
14	41	48.8	151	1	S30146		fasciclin I precur
15	41	48.8	339	2	JC5882		ribosomal protein
16	41	48.8	349	2	JC5881		myocyte enhancer f
17	41	48.8	411	2	AE2152		two-component sens
18	41	48.8	707	2	F86925		probable acyl-CoA
19	41	48.8	967	2	S58360		antibiotic Pep5 b
20	41	48.8	975	2	T03004		hydroxyribonuclea
21	41	48.8	1172	2	T00065		hypothetical prote
22	41	48.8	1559	2	T07757		probable DNA (cyto
23	40	47.6	97	2	S59888		C4 protein - tomat
24	40	47.6	205	2	S26854		microfilarial sheat
25	40	47.6	205	2	A40525		proline-rich sheat
26	40	47.6	209	2	T43565		type III secretion
27	40	47.6	209	2	B40049		virC-region hypoth
28	40	47.6	210	2	S21428		hypothetical prote
29	40	47.6	225	2	C70045		two-component resp

30	40	47.6	231	2	F69977	two-component resp
31	40	47.6	309	2	H72626	probable 2-oxoacid
32	40	47.6	337	2	A97084	uncharacterized pr
33	40	47.6	406	2	C83867	Xaa-Pro dipeptidas
34	40	47.6	422	2	D86446	hypothetical prote
35	40	47.6	560	2	T02404	probable beta-gluc
36	40	47.6	609	2	S65208	probable membrane
37	40	47.6	1184	2	D86387	probable protein P
38	40	47.6	1215	2	E70614	hypothetical prote
39	40	47.6	3570	2	T45025	mucin MUC5B, trach
40	39.5	47.0	365	2	F87552	dprA protein (impo
41	39.5	47.0	631	2	A57286	probable serine/th
42	39	46.4	242	2	AD1928	hypothetical prote
43	39	46.4	256	1	WNBEFN	28K protein - suid
44	39	46.4	258	2	T23957	hypothetical prote
45	39	46.4	268	2	S31010	gene 65 protein -

ALIGNMENTS

RESULT 1

A42013

alpha-1-B-glycoprotein - North American opossum (fragments)

C:Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opo

C:Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 31-Dec-1993

C:Accession: A42013

R:Catanesse, J.J.; Kress, L.F.

Biochemistry 31, 410-418, 1992

A:Title: Isolation from opossum serum of a metalloproteinase inhibitor homologous to

A:Reference number: A42013; MUID:92118834; PMID:1731898

A:Accession: A42013

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-237 <CAT>

A:Cross-references: GB:J05356

C:Keywords: glycoprotein

Query Match 75.0%; Score 63; DB 2; Length 237;

Best Local Similarity 80.0%; Pred. No. 0.0087;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy

1 LKAMDPTPLWKTE 15

||||| |||||

Db 1 LKAMDTPRLWIEE 15

RESULT 2

A54063

TATA-binding protein-associated factor II - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 21-Jul-2000

C:Accession: A54063

R:Verrijzer, C.P.; Yokomori, K.; Chen, J.L.; Tjian, R.

Science 264, 933-941, 1994

A:Title: Drosophila TAF-II 150: similarity to yeast gene TSM-1 and specific binding t

A:Reference number: A54063; MUID:94233377; PMID:8178153

A:Accession: A54063

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-1213 <VER>

A:Cross-references: GB:X79243; NID:g541664; PIDN:CAA55830.1; PID:g541665

C:Genetics:

A:Gene: Flybase:Taf150

A:Cross-references: Flybase:FBgn0011836

Query Match

Best Local Similarity 54.8%; Score 46; DB 2; Length 1213;

Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy

1 LKAMDPTPLWKTE 15

||||| |||||

Db 620 LSAMDSPVLWRLD 634

RESULT 3

EF5099
hypothetical protein PAB1590 - *Pyrococcus abyssi* (strain Orsay)
C:Species: *Pyrococcus abyssi*
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: E75099
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome structure
A:Reference number: A75001
A:Accession: E75099
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-695 <KAW>
A:Cross-references: GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB50098.1; PID:el51599
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB1590

Query Match 52.4%; Score 44; DB 2; Length 695;

Best Local Similarity 54.5%; Pred. No. 35;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 AMDPTPLWIK 13

Db 561 ANDPPPPWLE 571

RESULT 4

T38769
hypothetical protein SPAC3H8.11 - fission yeast (*Schizosaccharomyces pombe*)
C:Species: *Schizosaccharomyces pombe*
C>Date: 20-Oct-2000 #sequence_revision 08-Dec-2000 #text_change 08-Dec-2000
C:Accession: T38769; T38072
R:Gentiles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, January 1996
A:Reference number: Z21810
A:Accession: T38769
A:Molecule type: DNA
A:Residues: 1-105 <GEN>
A:Cross-references: EMBL:Z69086; NID:gl177658; PIDN:CAA93168.1; PID:gl177669; GSPDB:GN00
A:Experimental source: strain 972h; cosmid c3H8
R:Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, April 1996
A:Reference number: Z21767
A:Accession: T38072
A>Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 90-777 <CON>
A:Cross-references: EMBL:Z70690; NID:gl256511; PIDN:CAA94619.1; PID:g3859771; GSPDB:GN00
A:Experimental source: strain 972h; cosmid c1F3
C:Genetics:
A:Gene: spac1f3.01; SPDB:SPAC3H8.11; SPDB:SPAC1F3.01
A:Map position: 1

Query Match 52.4%; Score 44; DB 2; Length 777;

Best Local Similarity 46.2%; Pred. No. 39;

Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 AMDPTPLWIKTE 15

Db 212 SVDETEPIWSTE 224

RESULT 5

T09402
immunoglobulin-like protein IGSF1 - human
C:Species: *Homo sapiens* (man)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: T09402
R:Mazzarella, R.; Pengue, G.; Jones, J.; Jones, C.; Schlessinger, D.

Genomics 48, 157-162, 1998

A:Title: Cloning and expression of an immunoglobulin superfamily gene (IGSF1) in Xq25
A:Reference number: Z16665; MUID:98190514; PMID:9521868

A:Accession: T09402

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-1327 <MAZ>

A:Cross-references: EMBL:AF034198; NID:g2645889; PIDN:AAC52057.1; PID:g2645890

C:Genetics:

A:Gene: igsf1

A:Map position: Xq25

Query Match 52.4%; Score 44; DB 2; Length 1327;

Best Local Similarity 63.6%; Pred. No. 72;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPTPLWIKT 14

Db 25 MDQPPELWIES 35

RESULT 6

AB0644
probable glycosyl hydrolase STY1249 [imported] - *Salmonella enterica* subsp. *enterica*
C:Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
A:Note: this species has also been called *Salmonella typhi*
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AB0644
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
th, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* se
A:Reference number: AB0502; PMID:11677608
A:Accession: AB0644
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-341 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD08333.1; PID:gi6502378; GSPDB:GN00176
C:Genetics:
A:Gene: STY1249

Query Match 51.2%; Score 43; DB 2; Length 341;

Best Local Similarity 47.1%; Pred. No. 23;

Matches 8; Conservative 3; Mismatches 2; Indels 4; Gaps 1;

QY 2 KAMDPTP---PLWIKT 14

Db 217 RAIDPRPAGSPYWLKT 233

RESULT 7

DB6314
hypothetical protein F2H15.14 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 30-Jun-2002
C:Accession: DB6314
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: AB6141; MUID:21016719; PMID:11130712
A:Accession: DB6314
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-687 <STO>

Query Match 51.2%; Score 43; DB 2; Length 341;

Best Local Similarity 47.1%; Pred. No. 23;

Matches 8; Conservative 3; Mismatches 2; Indels 4; Gaps 1;

QY 2 KAMDPTP---PLWIKT 14

Db 217 RAIDPRPAGSPYWLKT 233

A:Cross-references: GB:AE005172; NID:9665069; PIDN:AAF97271.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 51.2%; Score 43; DB 2; Length 687;

Best Local Similarity 46.7%; Pred. No. 50;

Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LKAMDTPPLWKTE 15

I : : |||||

Db 225 LRLQTNELWLKTD 239

RESULT 8

A31898

hydroxymethylglutaryl-CoA reductase (NADPH2) (EC 1.1.1.34) - sea urchin (Strongylocentrotus

C:Species: Strongylocentrotus purpuratus (purple urchin)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002

C:Accession: A31898; A28367

R:Woodward, H.D.; Allen, J.M.C.; Lennarz, W.J.

J. Biol. Chem. 263, 18411-18418, 1988

A:Title: 3-hydroxy-3-methylglutaryl-coenzyme A reductase of the sea urchin embryo. Deduced

A:Reference number: A31898; MUID:89054023; PMID:3192541

A:Accession: A31898

A:Molecule type: mRNA

A:Residues: 1-932 <WO2>

A:Cross-references: GB:J04200; NID:g161522; PIDN:AAA30060.1; PID:g161523

A:Note: the authors rearranged portions of the coding region in Figure 2, and the above

submitted to GenBank

A:Note: the authors translated the codon GGA for residue 805 as Glu

R:Woodward, H.D.; Allen, J.M.C.; Lennarz, W.J.

J. Biol. Chem. 263, 2513-2517, 1988

A:Title: 3-hydroxy-3-methylglutaryl coenzyme A reductase in the sea urchin embryo is dev

A:Reference number: A28367; MUID:88115403; PMID:3276692

A:Accession: A28367

A:Molecule type: mRNA

A:Residues: 689-735 <WO2>

C:Comment: This transmembrane glycoprotein of the endoplasmic reticulum is involved in t

C:Superfamily: hydroxymethylglutaryl-CoA reductase (NADPH)

C:Keywords: cholesterol biosynthesis; coenzyme A; endoplasmic reticulum; glycoprotein; N

F:279,850,886,930/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.2%; Score 43; DB 1; Length 932;

Best Local Similarity 70.0%; Pred. No. 70;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KAMDTPPLW 11

I : |||||

Db 298 KKIDPTMPLW 307

RESULT 9

D71194

hypothetical protein PH1828 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000

C:Accession: D71194

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A:Reference number: A71000; MUID:98344137; PMID:9679194

A:Accession: D71194

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-115 <KAW>

A:Cross-references: GB:AF000007; NID:g3236134; PIDN:BAA30947.1; PID:g3258264

A:Experimental source: strain OT3

A:Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A:Gene: PH1828

Query Match 50.0%; Score 42; DB 2; Length 115;

Best Local Similarity 66.7%; Pred. No. 9.8;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MDPpPLWI 12

I : |||||

Db 89 ISPSPLWI 97

RESULT 10

A81717

conserved hypothetical protein TC0306 [imported] - Chlamydia muridarum (strain Nigg)

C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000

C:Accession: A81717

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe

C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe

Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39

A:Reference number: A81500; MUID:20150255; PMID:10684935

A:Accession: A81717

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-398 <TET>

A:Cross-references: GB:AE002298; GB:AE002160; NID:g7190343; PIDN:AAF39171.1; PID:g719

A:Experimental source: strain Nigg (MoPn)

C:Genetics:

A:Gene: TC0306

C:Superfamily: Chlamydia trachomatis hypothetical protein CT036

Query Match 50.0%; Score 42; DB 2; Length 398;

Best Local Similarity 77.8%; Pred. No. 39;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMDTPPL 10

I : |||||

Db 309 KELDPTPL 317

RESULT 11

T04646

aspartate transaminase (EC 2.6.1.1) precursor, chloroplast - Arabidopsis thaliana

N:Alternate names: aspartate aminotransferase; protein F10N7.200

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1999

C:Accession: T04646; S56657; S47490

R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.

Submitted to the Protein Sequence Database, March 1999

A:Reference number: Z15263

A:Accession: T04646

A:Molecule type: DNA

A:Residues: 1-453 <BEV>

A:Cross-references: EMBL:AL021636

A:Experimental source: cultivar Columbia; BAC clone F10N7

R:Wilkie, S.E.; Roper, J.M.; Smith, A.G.; Warren, M.J.

Plant Mol. Biol. 27, 1227-1233, 1995

A:Title: Isolation, characterisation and expression of a cDNA clone encoding plastid

A:Reference number: S56657; MUID:95284373; PMID:7768905

A:Accession: S56657

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-21, 'NV', 24-453 <WIL>

A:Cross-references: EMBL:X81026; NID:g531554; PIDN:CAA56932.1; PID:g531555

C:Genetics:

A:Gene: aat1

A:Map position: 4

A:Genome: nuclear

A:Introns: 20/3; 37/3; 102/3; 115/3; 145/3; 182/1; 218/3; 266/3; 322/2; 410/3

A:Note: F10N7.200

C:Superfamily: aspartate aminotransferase

C:Keywords: aminotransferase; chloroplast;

F:298/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 50.0%; Score 42; DB 2; Length 453;
Best Local Similarity 60.0%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPTPLWIK 13
:||||| :|
Db 238 IDPTPEQWVK 247

RESULT 12

VHXPWV

major structural nucleoprotein - Machupo virus

N:Alternate names: nucleocapsid protein

C:Species: Machupo virus

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Jul-1999

C:Accession: S18042

R:Griffiths, C.; Wilson, S.M.; Clegg, J.C.S.

submitted to the EMBL Data Library, October 1991

A:Description: Sequence of the nucleocapsid gene of Machupo virus: close relationship with

A:Reference number: S18042

A:Accession: S18042

A:Molecule type: genomic RNA

A:Residues: 1-564 <GRI>

A:Cross-references: EMBL:X62616; NID:g60621; PIDN:CAA44486.1; PID:g60622

C:Genetics:

A:Map position: segment S

C:Superfamily: arenavirus major nucleoprotein

C:Keywords: nucleocapsid; nucleoprotein

Query Match 50.0%; Score 42; DB 1; Length 564;
Best Local Similarity 46.7%; Pred. No. 58;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWIKTE 15
:|:||||| :|
Db 368 VKKLDPTWTLWDIE 382

RESULT 13

A29900

fasciclin I precursor - American bird grasshopper

C:Species: Schistocerca americana (American bird grasshopper)

C:Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 01-Dec-2000

C:Accession: A29900; A31817

R:Zinn, K.; McAllister, L.; Goodman, C.S.

Cell 53, 577-587, 1988

A:Title: Sequence analysis and neuronal expression of fasciclin I in grasshopper and Dro

A:Reference number: A29900; MUID:88223351; PMID:3370670

A:Accession: A29900

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-662 <ZIN>

A:Cross-references: GB:M20544; GB:J03787; NID:g160846; PID:g160847

R:Snow, P.M.; Zinn, K.; Harrelson, A.L.; McAllister, L.; Schilling, J.; Bastiani, M.J.;

Proc. Natl. Acad. Sci. U.S.A. 85, 5291-5295, 1988

A:Title: Characterization and cloning of fasciclin I and fasciclin II glycoproteins in t

A:Reference number: A94202; MUID:88276943; PMID:2839842

A:Accession: A31817

A:Molecule type: mRNA

A:Residues: 25-42 <SNO>

A:Cross-references: EMBL:M20544; EMBL:J03787

Query Match 50.0%; Score 42; DB 2; Length 662;
Best Local Similarity 58.3%; Pred. No. 70;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWIK 12
:|:|:|||||
Db 104 LSELDGNPLWIK 115

RESULT 14

S30146

ribosomal protein S13, cytosolic - maize

C:Species: Zea mays (maize)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S30146

R:Joanin, P.; Gigot, C.; Philipps, G.

Plant Mol. Biol. 21, 701-704, 1993

A:Title: cDNA nucleotide sequence and expression of a maize cytoplasmic ribosomal pro

A:Reference number: S30146; MUID:93192530; PMID:8448368

A:Accession: S30146

A:Molecule type: mRNA

A:Residues: 1-151 <JOA>

A:Cross-references: EMBL:X62455; NID:g288058; PIDN:CAA44311.1; PID:g288059

C:Superfamily: rat ribosomal protein S13; eubacterial ribosomal protein S15 homology

C:Keywords: protein biosynthesis; ribosome

F:2-151/Product: ribosomal protein S13 #status predicted <MAT>

F:82-148/Domain: eubacterial ribosomal protein S15 homology <ES15>

Query Match 48.8%; Score 41; DB 1; Length 151;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 TPPLWIKT 14
:||||| :|
Db 21 TPPTWIKT 28

RESULT 15

JC5882

myocyte enhancer factor 2B-2 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 11-Mar-1998 #sequence_revision 11-Mar-1998 #text_change 16-Jul-1999

C:Accession: JC5882

R:Morisaki, T.; Sermsuvitayawong, K.; Byun, S.H.; Matsuda, Y.; Hidaka, K.; Morisaki,

J. Biochem. 122, 939-946, 1997

A:Title: Mouse Mef2b gene: Unique member of MEF2 gene family.

A:Reference number: JC5881; MUID:98104045; PMID:9443608

A:Accession: JC5882

A:Molecule type: DNA

A:Residues: 1-339 <MOR>

A:Cross-references: DDBJ:D87828

C:Comment: This factor plays a differentiation of myocytes, including cardiomyocytes.

C:Genetics:

A:Gene: Mef2b

A:Map position: 8

C:Superfamily: serum response factor DNA-binding domain homology

F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match

Best Local Similarity 48.8%; Score 41; DB 2; Length 339;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 AMDPTPLWIKTE 15
:||||| :|
Db 281 ASPPTPPVSIKSE 293

Search completed: June 27, 2003, 18:02:39
Job time : 16 secs